



A Genetic Algorithm for Scale-Based Translocon Simulation

Submitted by Emmanuel Lemoine on Mon, 10/06/2014 - 18:25

Titre	A Genetic Algorithm for Scale-Based Translocon Simulation
Type de publication	Communication
Type	Communication avec actes dans un congrès
Année	2012
Langue	Anglais
Date du colloque	2012
Titre du colloque	7th IAPR International Conference, PRIB 2012
Titre des actes ou de la revue	Pattern Recognition in Bioinformatics
Volume	7632
Pagination	26 - 37
Auteur	Laroum, Sami [1], Duval, Béatrice [2], Tessier, Dominique [3], Hao, Jin-Kao [4]
Pays	Japon
Editeur	Springer Berlin Heidelberg
Ville	Tokyo
ISBN	978-3-642-34122-9 / 978-3-642-34123-6
Mots-clés	algorithm analysis and problem complexity [5], Artificial Intelligence (incl. Robotics) [6], classification [7], Computational Biology/Bioinformatics [8], Data Mining and Knowledge Discovery [9], genetic algorithm [10], Health Informatics [11], Membrane Proteins [12], optimization [13], pattern recognition [14]
Résumé en anglais	Discriminating between secreted and membrane proteins is a challenging task. A recent and important discovery to understand the machinery responsible of the insertion of membrane proteins was the results of Hessa experiments [9]. The authors developed a model system for measuring the ability of insertion of engineered hydrophobic amino acid segments in the membrane. The main results of these experiments are summarized in a new "biological hydrophobicity scale". In this scale, each amino acid is represented by a curve that indicates its contribution to the process of protein insertion according to its position inside the membrane. We follow the same hypothesis as Hessa but we propose to determine "in silico" the hydrophobicity scale. This goal is formalized as an optimization problem, where we try to define a set of curves that gives the best discrimination between signal peptide and protein segments which cross the membrane. This paper describes the genetic algorithm that we developed to solve this problem and the experiments that we conducted to assess its performance.
Notes	Date du colloque : 11/2012
URL de la notice	http://okina.univ-angers.fr/publications/ua4483 [15]
DOI	10.1007/978-3-642-34123-6_3 [16]

Liens

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- [16] http://dx.doi.org/10.1007/978-3-642-34123-6_3

Publié sur *Okina* (<http://okina.univ-angers.fr>)